Attorney's Docket No.: 22477-708

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Patent Application of:

Eric Lietz

Application No.: 09/975,754

Filed: October 10, 2001

For: RANDOM TRUNCATION AND AMPLIFICATION OF NUCLEIC ACID

Group Art Unit: 1634

Examiner: A. Chakrabarti, Ph.D.

AMENDMENT UNDER 37 C.F.R. §1.111

Assistant Commissioner for Patents
Washington, D.C. 20231

Dear Sir:

This Amendment is in response to the Office Action mailed January 15, 2003. Applicants submit herewith a terminal disclaimer to overcome Examiner's nonstatutory double patenting rejection under 37 CFR 3.73(b). Reconsideration is respectfully requested in view of the following remarks.

In the Claims

Please add the following new claims 53-65:

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21 ~~53.~~ (New) The method according to claim 19 wherein the target sequence has a sequence which is at least partially unknown at the time of primer extension amplification.

22 ~~54.~~ (New) The method according to claim 19 wherein the first and second fixed sequences include at least one restriction site.

23 ~~55.~~ (New) The method according to claim 19 wherein one of the fixed sequence of the first and second primers includes an ATG or a GTA sequence and the fixed sequence of the other primer includes a sequence encoding one or more translation stop codons.

24 ~~56.~~ (New) The method according to claim 19 wherein the length of the first and second primers is between 10 and 80 nucleotides.

25 57. (New) The method according to claim 19 wherein the first or second unknown sequence has a length between 3 and 70 nucleotides.

26 58. (New) The method according to claim 19 wherein the first or second unknown sequence has a length between 4 and 50 nucleotides.

27 59. (New) The method according to claim 19 wherein the first or second unknown sequence has a length between 5 and 20 nucleotides.

B. Cont'd

28 60. (New) The method according to claim 19 wherein the first or second unknown sequence further includes a sequence encoding one or more specific amino acid residues.

29 61. (New) The method according to claim 28 wherein the one or more specific amino acid residues are conserved amino acid residues of the protein encoded by the target sequence.

30 62. (New) The method according to claim 19 wherein at least a portion of the multiple cycles of primer extension polymerase amplification is performed such that extension by the polymerase is at least partially performed at a temperature below 70°C for at least 30 sec.

31 63. (New) The method according to claim 19 wherein at least a portion of the multiple cycles of primer extension polymerase amplification is performed such that extension by the polymerase is at least partially performed at a temperature below 60°C for at least 30 sec.

32 64. (New) The method according to claim 19 wherein at least a portion of the multiple cycles of primer extension polymerase amplification is performed such that extension by the polymerase is at least partially performed at a temperature below 50°C for at least 30 sec.

33 65. (New) The method according to claim 19 wherein at least a portion of the one or more cycles of primer extension polymerase amplification is performed such that extension by the polymerase is at least partially performed by heating the amplification reaction mixture from temperature of between 30°C to 50°C to a temperature between 65°C to 75°C over the course of at least 30 sec.--